

RAW SEQUENCE LISTING

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Application Serial Number: 10/536,606
Source: PCT
Date Processed by STIC: 03/06/2006

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PCT

RAW SEQUENCE LISTING

DATE: 03/06/2006

PATENT APPLICATION: US/10/536,606

TIME: 15:17:43

Input Set : A:\25421-502NATL.txt

Output Set: N:\CRF4\03062006\J536606.raw

3 <110> APPLICANT: Cosson et al.
 5 <120> TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE
 7 <130> FILE REFERENCE: 25421-502NATL
 9 <140> CURRENT APPLICATION NUMBER: 10/536,606
 10 <141> CURRENT FILING DATE: 2005-05-26
 12 <150> PRIOR APPLICATION NUMBER: PCT/CH2003/00836
 13 <151> PRIOR FILING DATE: 2003-12-19
 15 <150> PRIOR APPLICATION NUMBER: 10/324,967
 16 <151> PRIOR FILING DATE: 2002-12-19
 18 <160> NUMBER OF SEQ ID NOS: 64
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1050
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Pseudomonas aeruginosa
 27 <400> SEQUENCE: 1

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30	atgcaggcgg	tcatgcgcca	gatcatgacc	gggcagtgc	ccgacgcgca	gatcggcgcc	120
32	ttcctgatgg	gcatgcggat	gaagagcgaa	accatcgacg	agatcgtcgg	cgcggtggcg	180
34	gtgatgcgcg	aactggccga	cggcgtgcag	ttgcctacgc	tgaagcatgt	ggtcgacgtg	240
36	gtcggcaccg	gcggcgatgg	cgcgaaacatc	ttcaacgtgt	cctcggcggc	gtccttcgtg	300
38	gtcgccgccc	ctggcgccaa	ggtcgccaaa	cacggtaacc	gcgcgggtctc	cggcaagagc	360
40	ggcagcgccc	acttgctgga	agccgcgggc	atctacctgg	agctgacctc	cgaacagggtg	420
42	gcgcgttgca	tcgacaccgt	cggcgtcggg	ttcatgttcg	cccagggtcca	ccacaaggcg	480
44	atgaagtacg	ccgccgggtcc	gcgcgcgcag	ctgggcttgc	ggactctgtt	caacatgctt	540
46	ggcccactga	ccaaccgggc	gggagtcagg	caccagggtg	tcgggggtgtt	caccaggaa	600
48	ctgtgcaagc	cgctggctga	agtgtcgaag	cgtctcgcca	gcgagcatgt	gctggtggtg	660
50	cattcgcgcg	acgggctgga	cgagttcagt	ctggccgcgg	cgaccacat	tgccgagttg	720
52	aaggacggcg	aggtacgcga	gtacgaagtg	cgtcccagg	acttcgggat	caagagccag	780
54	accctgatgg	ggctggaggt	cgacagtccg	caggcctcgc	tggaaactgat	ccgcgacgct	840
56	ttggggcggc	gcaagaccga	ggctgggcag	aaggccgcgc	agctgatcgt	gatgaatgcc	900
58	ggcccggcac	tgtacgctgc	cgatctggcg	accagcctgc	acgagggcat	tcaactggcc	960
60	cacgatgccc	tgcacaccgg	gctggcacgg	gagaagatgg	acgaactggg	ggccttcacc	1020
62	gccgtttaca	gagaggagaa	cgcacagtga				1050

65 <210> SEQ ID NO: 2
 66 <211> LENGTH: 349
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Pseudomonas aeruginosa
 70 <400> SEQUENCE: 2

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73	1				5					10					15	
76	Thr	Thr	Glu	Glu	Met	Gln	Ala	Val	Met	Arg	Gln	Ile	Met	Thr	Gly	Gln
77					20					25				30		

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80 Cys Thr Asp Ala Gln Ile Gly Ala Phe Leu Met Gly Met Arg Met Lys
81      35      40      45
84 Ser Glu Thr Ile Asp Glu Ile Val Gly Ala Val Ala Val Met Arg Glu
85      50      55      60
88 Leu Ala Asp Gly Val Gln Leu Pro Thr Leu Lys His Val Val Asp Val
89 65      70      75      80
92 Val Gly Thr Gly Gly Asp Gly Ala Asn Ile Phe Asn Val Ser Ser Ala
93      85      90      95
96 Ala Ser Phe Val Val Ala Ala Ala Gly Gly Lys Val Ala Lys His Gly
97      100      105      110
100 Asn Arg Ala Val Ser Gly Lys Ser Gly Ser Ala Asp Leu Leu Glu Ala
101      115      120      125
104 Ala Gly Ile Tyr Leu Glu Leu Thr Ser Glu Gln Val Ala Arg Cys Ile
105      130      135      140
108 Asp Thr Val Gly Val Gly Phe Met Phe Ala Gln Val His His Lys Ala
109 145      150      155      160
112 Met Lys Tyr Ala Ala Gly Pro Arg Arg Glu Leu Gly Leu Arg Thr Leu
113      165      170      175
116 Phe Asn Met Leu Gly Pro Leu Thr Asn Pro Ala Gly Val Arg His Gln
117      180      185      190
120 Val Val Gly Val Phe Thr Gln Glu Leu Cys Lys Pro Leu Ala Glu Val
121      195      200      205
124 Leu Lys Arg Leu Gly Ser Glu His Val Leu Val Val His Ser Arg Asp
125      210      215      220
128 Gly Leu Asp Glu Phe Ser Leu Ala Ala Ala Thr His Ile Ala Glu Leu
129 225      230      235      240
132 Lys Asp Gly Glu Val Arg Glu Tyr Glu Val Arg Pro Glu Asp Phe Gly
133      245      250      255
136 Ile Lys Ser Gln Thr Leu Met Gly Leu Glu Val Asp Ser Pro Gln Ala
137      260      265      270
140 Ser Leu Glu Leu Ile Arg Asp Ala Leu Gly Arg Arg Lys Thr Glu Ala
141      275      280      285
144 Gly Gln Lys Ala Ala Glu Leu Ile Val Met Asn Ala Gly Pro Ala Leu
145      290      295      300
148 Tyr Ala Ala Asp Leu Ala Thr Ser Leu His Glu Gly Ile Gln Leu Ala
149 305      310      315      320
152 His Asp Ala Leu His Thr Gly Leu Ala Arg Glu Lys Met Asp Glu Leu
153      325      330      335
156 Val Ala Phe Thr Ala Val Tyr Arg Glu Glu Asn Ala Gln
157      340      345
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 918
162 <212> TYPE: DNA
163 <213> ORGANISM: Pseudomonas aeruginosa
165 <400> SEQUENCE: 3
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168 gaggtggccg ccgagttcga taacccggtg atgctgtact cgatcggcaa ggattccgcg      120
170 gtcatgctgc acctggcccc caaggccttc ttccccggca agctgccctt cccggtgatg      180
172 cacgtggaca cccgctggaa attccaggag atgtacaggt tccgtgatcg gatggtcgag      240

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174 gaaatggggcc tggatctgat caccacgctc aaccgggacg gcgtcgccca gggcatcaac 300
176 ccgttcaccc acggcagcgc caagcacacc gacgtgatga agaccgaggg actcaagcag 360
178 gccctggaca agtacggttt cgacgtgcc ttcggcggtg cgcgccgga cgaggagaag 420
180 tcgcgggcca aggaacgggt ctattcggtc cgcgacagca agcaccgctg ggaccgaag 480
182 aaccagcgtc ccgagctgtg gaacatctac aacggcaagg tgaagaagg cgagtcgac 540
184 cgcgtcttcc cgctgtccaa ctggaccgag ctggacatct ggcaatacat ctacctggaa 600
186 ggcattcccga tcgtcccgt gtacttcgcc gccgagcgcg aggtcatcga gaagaatggc 660
188 acattgatca tgatcgacga cgagcgcac ctcgagcatc tctctgacga agagaaagcc 720
190 cgcattcaga agcgcattgt gcgttccgt accctcggct gctaccgct caccggcgcg 780
192 gtcgagtcca gcgccaccac gctgccgaa atcatccagg aaatgctcct gacgcgtact 840
194 tccgaacgcc agggccgggt catcgaccat gaccaggccg gttcgatgga agaaaagaaa 900
196 cgtcagggt atttctga 918
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 305
201 <212> TYPE: PRT
202 <213> ORGANISM: Pseudomonas aeruginosa
204 <400> SEQUENCE: 4
206 Met Val Asp Lys Leu Thr His Leu Lys Gln Leu Glu Ala Glu Ser Ile
207 1 5 10 15
210 His Ile Ile Arg Glu Val Ala Ala Glu Phe Asp Asn Pro Val Met Leu
211 20 25 30
214 Tyr Ser Ile Gly Lys Asp Ser Ala Val Met Leu His Leu Ala Arg Lys
215 35 40 45
218 Ala Phe Phe Pro Gly Lys Leu Pro Phe Pro Val Met His Val Asp Thr
219 50 55 60
222 Arg Trp Lys Phe Gln Glu Met Tyr Arg Phe Arg Asp Arg Met Val Glu
223 65 70 75 80
226 Glu Met Gly Leu Asp Leu Ile Thr His Val Asn Pro Asp Gly Val Ala
227 85 90 95
230 Gln Gly Ile Asn Pro Phe Thr His Gly Ser Ala Lys His Thr Asp Val
231 100 105 110
234 Met Lys Thr Glu Gly Leu Lys Gln Ala Leu Asp Lys Tyr Gly Phe Asp
235 115 120 125
238 Ala Ala Phe Gly Gly Ala Arg Asp Glu Glu Lys Ser Arg Ala Lys
239 130 135 140
242 Glu Arg Val Tyr Ser Phe Arg Asp Ser Lys His Arg Trp Asp Pro Lys
243 145 150 155 160
246 Asn Gln Arg Pro Glu Leu Trp Asn Ile Tyr Asn Gly Lys Val Lys Lys
247 165 170 175
250 Gly Glu Ser Ile Arg Val Phe Pro Leu Ser Asn Trp Thr Glu Leu Asp
251 180 185 190
254 Ile Trp Gln Tyr Ile Tyr Leu Glu Gly Ile Pro Ile Val Pro Leu Tyr
255 195 200 205
258 Phe Ala Ala Glu Arg Glu Val Ile Glu Lys Asn Gly Thr Leu Ile Met
259 210 215 220
262 Ile Asp Asp Glu Arg Ile Leu Glu His Leu Ser Asp Glu Glu Lys Ala
263 225 230 235 240
266 Arg Ile Glu Lys Arg Met Val Arg Phe Arg Thr Leu Gly Cys Tyr Pro
267 245 250 255

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270 Leu Thr Gly Ala Val Glu Ser Ser Ala Thr Thr Leu Pro Glu Ile Ile
271          260          265          270
274 Gln Glu Met Leu Leu Thr Arg Thr Ser Glu Arg Gln Gly Arg Val Ile
275          275          280          285
278 Asp His Asp Gln Ala Gly Ser Met Glu Glu Lys Lys Arg Gln Gly Tyr
279          290          295          300
282 Phe
283 305
286 <210> SEQ ID NO: 5
287 <211> LENGTH: 822
288 <212> TYPE: DNA
289 <213> ORGANISM: Pseudomonas aeruginosa
291 <400> SEQUENCE: 5
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294 ctgccgcact ggcgcgccga cgtggtggtg cgctcgaagg ccgacgaatc gccggtgact      120
296 gccgccgacc tggccgcgca ccatatattg gaggcgggat tgcgggcgct ggcgccggac      180
298 attccggtgc ttccgaaga ggattgcgag ataccgctga gcgagcgcgg cactggcggg      240
300 cgctggtggc tgggtggacc gctggacggc accaaggagt tcattctcgg tagcgaggag      300
302 ttcaccgtca acgtggccct ggtcgaggat ggccgggtgc tgttcggcct ggtcggcggtg      360
304 ccggtgagcg gccgctgcta ctacggtggc gccggtctcg gtgcctggcg cgaggaggcc      420
306 gatggccgcg cgcaaccgat cagtgtgcgc ctggagcccc aggaggcctt caccgtggtg      480
308 gccagcaagc gccatggcag cccggcccag gagcgctgc tggatggctt gagcgagcgc      540
310 ttcggcgacc tgcggcgagc cagcatcggc agttcgctga agttctgcct gctggccgag      600
312 ggcgctgccg actgctatcc gcgcctgacg ccaacctcgc aatgggacac ggccgccgcc      660
314 cagggtgtgc tgggaaggcg cggcggcgag gtgctcgacc tgcattggtg gccattcacc      720
316 tacgagccgc gcgaggatta cctcaacggc tccttctctg ccctgccgcg cgccgccgag      780
318 tggcgagcgc agctgatcca actggcgcgc gcgctgcact ga      822
321 <210> SEQ ID NO: 6
322 <211> LENGTH: 273
323 <212> TYPE: PRT
324 <213> ORGANISM: Pseudomonas aeruginosa
326 <400> SEQUENCE: 6
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329 1          5          10          15
332 Gly Glu Ala Ile Leu Pro His Trp Arg Ala Asp Val Val Val Arg Ser
333          20          25          30
336 Lys Ala Asp Glu Ser Pro Val Thr Ala Ala Asp Leu Ala Ala His His
337          35          40          45
340 Ile Leu Glu Ala Gly Leu Arg Ala Leu Ala Pro Asp Ile Pro Val Leu
341          50          55          60
344 Ser Glu Glu Asp Cys Glu Ile Pro Leu Ser Glu Arg Gly His Trp Arg
345 65          70          75          80
348 Arg Trp Trp Leu Val Asp Pro Leu Asp Gly Thr Lys Glu Phe Ile Ser
349          85          90          95
352 Gly Ser Glu Glu Phe Thr Val Asn Val Ala Leu Val Glu Asp Gly Arg
353          100          105          110
356 Val Leu Phe Gly Leu Val Gly Val Pro Val Ser Gly Arg Cys Tyr Tyr
357          115          120          125
360 Gly Gly Ala Gly Leu Gly Ala Trp Arg Glu Glu Ala Asp Gly Arg Ala

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361      130      135      140
364 Gln Pro Ile Ser Val Arg Leu Glu Pro Glu Glu Ala Phe Thr Val Val
365 145      150      155      160
368 Ala Ser Lys Arg His Gly Ser Pro Ala Gln Glu Arg Leu Leu Asp Gly
369      165      170      175
372 Leu Ser Glu Arg Phe Gly Asp Leu Arg Arg Ala Ser Ile Gly Ser Ser
373      180      185      190
376 Leu Lys Phe Cys Leu Leu Ala Glu Gly Ala Ala Asp Cys Tyr Pro Arg
377      195      200      205
380 Leu Thr Pro Thr Ser Gln Trp Asp Thr Ala Ala Ala Gln Gly Val Leu
381      210      215      220
384 Glu Gly Ala Gly Gly Glu Val Leu Asp Leu His Gly Ala Pro Phe Thr
385 225      230      235      240
388 Tyr Glu Pro Arg Glu Asp Tyr Leu Asn Gly Ser Phe Leu Ala Leu Pro
389      245      250      255
392 Arg Ala Ala Glu Trp Arg Ser Glu Leu Ile Gln Leu Ala Arg Ala Leu
393      260      265      270
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401 <211> LENGTH: 1299
402 <212> TYPE: DNA
403 <213> ORGANISM: Pseudomonas aeruginosa
405 <400> SEQUENCE: 7
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408 cgtgccgggt tcgaggtggt ggtgggtcgac cgtcaggacg gtcccgcgct ggaaaccagc 120
410 ttcgccaacg ccggccaggt gtctcccggc tacgcttcgc cctgggcagc cccgggcatt 180
412 cccctgaagg ccatgaagtg gctgctggaa aagcacgcgc cgctggccat caagctcacc 240
414 tccgatccca gccagtacgc ctggatgctg cagatgctgc gcaactgcac cgccgagcgc 300
416 tacgccgtga acaaggagcg catgggtccgc ctgtccgagt acagccgcga ttgcctcgac 360
418 gaactgcgcg ccgagaccgg catcgccctac gagggccgca ccctcggcac caccctaactg 420
420 ttccgcaccc aggcgcagct ggacgccgcc ggcaaggaca tcgccgtgct cgagcgctcc 480
422 ggcgtgccct acgaggttct cgaccgcgac ggcacgcgcc gcgtagagcc ggctttggcc 540
424 aaggtcgccg acaagctggt cggcgccctt cgccctgccc acgaccagac cggcgactgc 600
426 cagctgttca ccaccgcct ggcggaatg gccaaaggcc tgggcgtgga gttccgcttc 660
428 ggccagaaca tcgagcgctt ggacttcgcc ggcgaccgca tcaacggcgt gctggtcaac 720
430 ggcgaattgc tcaccgccga ccactacgtg ctggccctgg gcagctactc gccgcaactg 780
432 ctcaagccgc tgggtatcaa ggctccggtc tatccgctga agggttattc gctgaccgtg 840
434 ccgatcacca acccgagat ggcgccgacc tcgaacatcc tcgacgagac ctacaagggtg 900
436 gcgatcaccc gcttcgacca gcgcacccgc gtccggcgca tggcggaat cgccggcttc 960
438 gacctgtcgc tgaaccgcgc ccgcgcgag accctggaaa tgatcaccac cgacctctat 1020
440 cccgagggcg gcgatatcag ccaggcgacc ttctggaccg gcctgcgcc ggcgaccccg 1080
442 gatggcacc cgatcgctcg cgccaccgc taccgcaacc tgttctctca taccggccac 1140
444 ggcaccctgg gttggacat ggccctgcgg tcgggtcgct acctggccga cctgatggcg 1200
446 aagaagcgcc cgcagatcag taccgaaggc ctggatattt cccgctacag caattccccg 1260
448 gagaacgcca agaatgccca tccagcgcca gcacactaa 1299
451 <210> SEQ ID NO: 8
452 <211> LENGTH: 432
453 <212> TYPE: PRT
454 <213> ORGANISM: Pseudomonas aeruginosa

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; N Pos. 85,88,174,175,245,293,319,325

VERIFICATION SUMMARY

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Input Set : A:\25421-502NATL.txt

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L:4828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:60

M:341 Repeated in SeqNo=37